

\*\*\*\*\* STN Columbus \*\*\*\*\*

FILE 'HOME' ENTERED AT 17:34:33 ON 04 AUG 2004

=> FILE BIOSIS, CABA, CAPLUS, EMBASE, JAPIO, LIFESCI, MEDLINE, SCISEARCH, USPATFULL

=> e fraser claire m/au

E1 3 FRASER CIRA/AU  
E2 21 FRASER CLAIRE/AU  
E3 704 --> FRASER CLAIRE M/AU  
E4 4 FRASER CLAIRE MARIE/AU  
E5 1 FRASER CLARE/AU  
E6 4 FRASER CLARE M/AU  
E7 2 FRASER CLARENCE/AU  
E8 4 FRASER CLARENCE F/AU  
E9 1 FRASER CLARENCE L/AU  
E10 2 FRASER CLARKE/AU  
E11 1 FRASER CLARKE F/AU  
E12 2 FRASER COLIN/AU

=> s e2-e4 and borrel?

L1 12 ("FRASER CLAIRE"/AU OR "FRASER CLAIRE M"/AU OR "FRASER CLAIRE MARIE"/AU) AND BORREL?

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 8 DUP REM L1 (4 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 8 ANSWERS - CONTINUE? Y/(N):y

L2 ANSWER 1 OF 8 MEDLINE on STN

AN 2004187163 MEDLINE

DN PubMed ID: 15064399

TI Comparison of the genome of the oral pathogen *Treponema denticola* with other spirochete genomes.

AU Seshadri Rekha; Myers Garry S A; Tettelin Herve; Eisen Jonathan A; Heidelberg John F; Dodson Robert J; Davidsen Tanja M; DeBoy Robert T; Fouts Derrick E; Haft Dan H; Selengut Jeremy; Ren Qinghu; Brinkac Lauren M; Madupu Ramana; Kolonay Jamie; Durkin Scott A; Daugherty Sean C; Shetty Jyoti; Shvartsbeyn Alla; Gebregeorgis Elizabeth; Geer Keita; Tsegaye Getahun; Malek Joel; Ayodeji Bola; Shatsman Sofiya; McLeod Michael P; Smajis David; Howell Jerrilyn K; Pal Sangita; Amin Anita; Vashisth Pankaj; McNeill Thomas Z; Xiang Qin; Sodergren Erica; Baca Ernesto; Weinstock George M; Norris Steven J; \*\*\*Fraser Claire M\*\*\*; Paulsen Ian T

CS The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850, USA.

NC R01-DE12488 (NIDCR)

SO Proceedings of the National Academy of Sciences of the United States of America, (2004 Apr 13) 101 (15) 5646-51.  
Journal code: 7505876. ISSN: 0027-8424.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-AE017226

EM 200405

ED Entered STN: 20040415

Last Updated on STN: 20040520

Entered Medline: 20040519

AB We present the complete 2,843,201-bp genome sequence of *Treponema denticola* (ATCC 35405) an oral spirochete associated with periodontal disease. Analysis of the *T. denticola* genome reveals factors mediating coaggregation, cell signaling, stress protection, and other competitive and cooperative measures, consistent with its pathogenic nature and lifestyle within the mixed-species environment of subgingival dental plaque. Comparisons with previously sequenced spirochete genomes revealed specific factors contributing to differences and similarities in spirochete physiology as well as pathogenic potential. The *T. denticola* genome is considerably larger in size than the genome of the related syphilis-causing spirochete *Treponema pallidum*. The differences in gene content appear to be attributable to a combination of three phenomena: genome reduction, lineage-specific expansions, and horizontal gene transfer. Genes lost due to reductive evolution appear to be largely

involved in metabolism and transport, whereas some of the genes that have arisen due to lineage-specific expansions are implicated in various pathogenic interactions, and genes acquired via horizontal gene transfer are largely phage-related or of unknown function.

L2 ANSWER 2 OF 8 USPATFULL on STN

AN 2003:244254 USPATFULL

TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof

IN \*\*\*Fraser, Claire M.\*\*\*, Potomac, MD, UNITED STATES

Adams, Mark D., Rockville, MD, UNITED STATES

Gocayne, Jeannine D., Potomac, MD, UNITED STATES

Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES

Smith, Hamilton O., Reisterstown, MD, UNITED STATES

Venter, J. Craig, Queenstown, MD, UNITED STATES

White, Owen R., Rockville, MD, UNITED STATES

PA Johns Hopkins University, Baltimore, MD (U.S. corporation)

PI US 2003170663 A1 20030911

AI US 2002-205220 A1 20020726 (10)

RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING  
Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995,  
PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun  
1995, ABANDONED

DT Utility

FS APPLICATION

LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850

CLMN Number of Claims: 19

ECL Exemplary Claim: 1

DRWN 23 Drawing Page(s)

LN.CNT 6270

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L2 ANSWER 3 OF 8 USPATFULL on STN

AN 2003:81597 USPATFULL

TI Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof

IN \*\*\*Fraser, Claire M.\*\*\*, Potomac, MD, United States

Adams, Mark D., N. Potomac, MD, United States

Gocayne, Jeannine D., Silver Spring, MD, United States

Hutchison, III, Clyde A., Chapel Hill, NC, United States

Smith, Hamilton O., Towson, MD, United States

Venter, J. Craig, Potomac, MD, United States

White, Owen, Gaithersburg, MD, United States

PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)

Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)

The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)

PI US 6537773 B1 20030325

AI US 1995-545528 19951019 (8)

RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995,  
now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on  
7 Jun 1995, now abandoned

DT Utility

FS GRANTED

EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard

LREP Human Genome Sciences, Inc.

CLMN Number of Claims: 44  
ECL Exemplary Claim: 1  
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)  
LN.CNT 15190

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the nucleotide sequence of the entire genome of *Mycoplasma genitalium*, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the *Mycoplasma genitalium* genome.

L2 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 1

AN 2000:254050 BIOSIS

DN PREV200000254050

TI Distribution of twelve linear extrachromosomal DNAs in natural isolates of Lyme disease spirochetes.

AU Palmer, Nanette; \*\*\*Fraser, Claire\*\*\* ; Casjens, Sherwood [Reprint author]

CS Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA

SO Journal of Bacteriology, (May, 2000) Vol. 182, No. 9, pp. 2476-2480. print.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 21 Jun 2000

Last Updated on STN: 5 Jan 2002

AB We have analyzed a panel of independent North American isolates of the Lyme disease agent spirochete, \*\*\**Borrelia*\*\*\* burgdorferi (sensu stricto), for the presence of linear plasmids with sequence similarities to the 12 linear plasmids present in the *B. burgdorferi* type strain, isolate B31. The frequency of similarities to probes from each of the 12 B31 plasmids varied from 13 to 100% in the strain panel examined, and these similarities usually reside on plasmids similar in size to the cognate B31 plasmid. Sequences similar to 5 of the 12 B31 plasmids were found in all of the isolates examined, and >66% of the panel members hybridized to probes from 4 other plasmids. Sequences similar to most of the *B. burgdorferi* B31 plasmid-derived DNA probes used were also found on linear plasmids in the related Eurasian Lyme agents \*\*\**Borrelia*\*\*\* garinii and \*\*\**Borrelia*\*\*\* afzelii; however, some of these plasmids had uniform but substantially different sizes from their *B. burgdorferi* counterparts.

L2 ANSWER 5 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 2

AN 2000:123164 BIOSIS

DN PREV200000123164

TI A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete \*\*\**Borrelia*\*\*\* burgdorferi.

AU Casjens, Sherwood [Reprint author]; Palmer, Nanette; van Vugt, Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; Lathigra, Raju; Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel; Hickey, Erin; Gwinn, Michelle; White, Owen; \*\*\*Fraser, Claire M.\*\*\*

CS Division of Molecular Biology and Genetics, Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA

SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.  
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 5 Apr 2000

Last Updated on STN: 3 Jan 2002

AB We have determined that \*\*\*Borrelia\*\*\* burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside \*\*\*Borrelia\*\*\*, suggesting that they perform specialized functions.

L2 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic fragments and open reading frames

IN \*\*\*Fraser, Claire\*\*\* ; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI US 1997-50359P	P	19970620		
US 1997-53344P	P	19970722		
US 1997-53377P	P	19970722		
US 1997-57483P	P	19970903		
WO 1998-US12764	W	19980618		

AB The present invention provides the complete nucleotide sequence of the \*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known

gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 3

AN 1998:361763 BIOSIS

DN PREV199800361763

TI Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.

AU \*\*\*Fraser, Claire M.\*\*\* [Reprint author]; Norris, Steven J.;  
Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert;  
Gwinn, Michelle; Hickey, Erin K.; Clayton, Rebecca; Ketchum, Karen A.;  
Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven;  
Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.;  
Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach,  
Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland,  
Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina;  
Weidman, Janice; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388.  
print.

CODEN: SCIEAS. ISSN: 0036-8075.

DT Article

LA English

ED Entered STN: 27 Aug 1998

Last Updated on STN: 27 Aug 1998

AB The complete genome sequence of *Treponema pallidum* was determined and shown to be 1,138,006 base pairs containing 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The number of identifiable transporters is small, and no phosphoenolpyruvate: phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the *T. pallidum* genome sequence with that of another pathogenic spirochete, \*\*\**Borrelia*\*\*\* burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L2 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 4

AN 1998:46985 BIOSIS

DN PREV19980046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\**Borrelia*\*\*\*  
burgdorferi.

AU \*\*\*Fraser, Claire M.\*\*\* [Reprint author]; Casjens, Sherwood; Huang,  
Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White,  
Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle;  
Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson,  
Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John;  
Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams,  
Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey,  
Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey;  
Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch,  
Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.

CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\*Borrelia\*\*\* burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e white owen r/au

E1	1	WHITE OWEN L/AU
E2	1	WHITE OWEN LISTER/AU
E3	20	--> WHITE OWEN R/AU
E4	3	WHITE OWEN RICHARDSON/AU
E5	1524	WHITE P/AU
E6	432	WHITE P A/AU
E7	1	WHITE P A B/AU
E8	30	WHITE P A E/AU
E9	16	WHITE P A F/AU
E10	1	WHITE P A S/AU
E11	41	WHITE P B/AU
E12	1	WHITE P B D/AU

=> s e3-e4 and borrel?

L3 3 ("WHITE OWEN R"/AU OR "WHITE OWEN RICHARDSON"/AU) AND BORREL?

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 3 DUP REM L3 (0 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L4 ANSWER 1 OF 3 USPATFULL on STN

AN 2003:244254 USPATFULL

TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof

IN Fraser, Claire M., Potomac, MD, UNITED STATES

Adams, Mark D., Rockville, MD, UNITED STATES

Gocayne, Jeannine D., Potomac, MD, UNITED STATES

Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES

Smith, Hamilton O., Reisterstown, MD, UNITED STATES

Venter, J. Craig, Queenstown, MD, UNITED STATES

\*\*\*White, Owen R.\*\*\*, Rockville, MD, UNITED STATES

PA Johns Hopkins University, Baltimore, MD (U.S. corporation)

PI US 2003170663 A1 20030911

AI US 2002-205220 A1 20020726 (10)

RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING  
Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995,  
PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun  
1995, ABANDONED

DT Utility

FS APPLICATION

LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850

CLMN Number of Claims: 19

ECL Exemplary Claim: 1

DRWN 23 Drawing Page(s)

LN.CNT 6270

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L4 ANSWER 2 OF 3 USPATFULL on STN

AN 2003:6806 USPATFULL

TI Selected polynucleotide and polypeptide sequences of the methanogenic archaeon, methanococcus jannashii

IN Bult, Carol J., Bar Harbor, ME, United States

\*\*\*White, Owen R.\*\*\*, Gaithersburg, MD, United States

Smith, Hamilton O., Baltimore, MD, United States

Woese, Carl R., Urbana, IL, United States

Venter, J. Craig, Rockville, MD, United States

PA The Board of Trustees of the University of Illinois, Urbana, IL, United States (U.S. corporation)

The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)

Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)

PI US 6503729 B1 20030107

AI US 1997-916421 19970822 (8)

PRAI US 1996-24428P 19960822 (60)

DT Utility

FS GRANTED

EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard

LREP Human Genome Sciences, Inc.

CLMN Number of Claims: 107

ECL Exemplary Claim: 1

DRWN 2 Drawing Figure(s); 2 Drawing Page(s)

LN.CNT 4244

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present application describes selected polynucleotide sequence from the 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements.

L4 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic fragments and open reading frames

IN Fraser, Claire; \*\*\*White, Owen R.\*\*\*; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9858943	A1	19981230	WO 1998-US12764	19980618
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2304925	AA	19981230	CA 1998-2304925	19980618

AU 9881534 A1 19990104 AU 1998-81534 19980618  
EP 1012157 A1 20000628 EP 1998-931389 19980618  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,  
IE, FI

PRAI US 1997-50359P P 19970620  
US 1997-53344P P 19970722  
US 1997-53377P P 19970722  
US 1997-57483P P 19970903  
WO 1998-US12764 W 19980618

AB The present invention provides the complete nucleotide sequence of the  
\*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the  
majority of the sequence of the B. burgdorferi extrachromosomal elements.  
Also provided are polypeptide sequences encoded by the polynucleotide  
sequences, corresponding polynucleotides and polypeptides, vectors and  
hosts comprising the polynucleotides, and assays and other uses thereof.  
Each open reading frame is identified with a function by homol. to a known  
gene or polypeptide. The present invention further demonstrates that a  
large sequence can be sequenced using a random approach, eliminating the  
up front cost of isolating and ordering overlapping or contiguous  
subclones prior to the start of the sequencing protocols. The present  
invention further provides polynucleotide and polypeptide sequence  
information stored on computer readable media, and computer-based systems  
and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> e clayton rebecca/au

E1 19 CLAYTON RAYMOND B/AU  
E2 1 CLAYTON REBECA/AU  
E3 13 --> CLAYTON REBECCA/AU  
E4 23 CLAYTON REBECCA A/AU  
E5 2 CLAYTON REG F/AU  
E6 1 CLAYTON REGINAL F/AU  
E7 14 CLAYTON REGINALD F/AU  
E8 1 CLAYTON REX/AU  
E9 27 CLAYTON RICHARD/AU  
E10 10 CLAYTON RICHARD A/AU  
E11 1 CLAYTON RICHARD ANTHONY/AU  
E12 3 CLAYTON RICHARD B/AU

=> s e2-e4 and borrel?

L5 5 ("CLAYTON REBECA"/AU OR "CLAYTON REBECCA"/AU OR "CLAYTON REBECCA  
A"/AU) AND BORREL?

=> dup rem l5

PROCESSING COMPLETED FOR L5

L6 3 DUP REM L5 (2 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L6 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic  
fragments and open reading frames

IN Fraser, Claire; White, Owen R.; \*\*\*Clayton, Rebecca\*\*\* ; Dougherty,  
Brian A.; Lathigra, Raju; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 9858943 A1 19981230 WO 1998-US12764 19980618  
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,  
DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,  
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,  
UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,  
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,  
CM, GA, GN, ML, MR, NE, SN, TD, TG  
CA 2304925 AA 19981230 CA 1998-2304925 19980618  
AU 9881534 A1 19990104 AU 1998-81534 19980618  
EP 1012157 A1 20000628 EP 1998-931389 19980618  
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,  
IE, FI

PRAI US 1997-50359P P 19970620  
US 1997-53344P P 19970722  
US 1997-53377P P 19970722  
US 1997-57483P P 19970903  
WO 1998-US12764 W 19980618

AB The present invention provides the complete nucleotide sequence of the  
\*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the  
majority of the sequence of the B. burgdorferi extrachromosomal elements.  
Also provided are polypeptide sequences encoded by the polynucleotide  
sequences, corresponding polynucleotides and polypeptides, vectors and  
hosts comprising the polynucleotides, and assays and other uses thereof.  
Each open reading frame is identified with a function by homol. to a known  
gene or polypeptide. The present invention further demonstrates that a  
large sequence can be sequenced using a random approach, eliminating the  
up front cost of isolating and ordering overlapping or contiguous  
subclones prior to the start of the sequencing protocols. The present  
invention further provides polynucleotide and polypeptide sequence  
information stored on computer readable media, and computer-based systems  
and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 1

AN 1998:361763 BIOSIS

DN PREV199800361763

TI Complete genome sequence of Treponema pallidum, the syphilis spirochete.

AU Fraser, Claire M. [Reprint author]; Norris, Steven J.; Weinstock, George  
M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle;  
Hickey, Erin K.; \*\*\*Clayton, Rebecca\*\*\*; Ketchum, Karen A.; Sodergren,  
Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson,  
Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.;  
Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach,  
Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland,  
Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina;  
Weidman, Janice; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388.  
print.

CODEN: SCIEAS. ISSN: 0036-8075.

DT Article

LA English

ED Entered STN: 27 Aug 1998

Last Updated on STN: 27 Aug 1998

AB The complete genome sequence of Treponema pallidum was determined and  
shown to be 1,138,006 base pairs containing 1041 predicted coding  
sequences (open reading frames). Systems for DNA replication,  
transcription, translation, and repair are intact, but catabolic and  
biosynthetic activities are minimized. The number of identifiable  
transporters is small, and no phosphoenolpyruvate: phosphotransferase  
carbohydrate transporters were found. Potential virulence factors include  
a family of 12 potential membrane proteins and several putative  
hemolysins. Comparison of the T. pallidum genome sequence with that of

another pathogenic spirochete, \*\*\*Borrelia\*\*\* burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L6 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 2

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\*Borrelia\*\*\*  
burgdorferi.

AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun;  
Sutton, Granger G.; \*\*\*Clayton, Rebecca\*\*\* ; Lathigra, Raju; White,  
Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle;  
Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson,  
Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John;  
Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams,  
Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey,  
Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey;  
Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch,  
Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.  
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\*Borrelia\*\*\* burgdorferi B31, the  
aetiologic agent of Lyme disease, contains a linear chromosome of 910,725  
base pairs and at least 17 linear and circular plasmids with a combined  
size of more than 533,000 base pairs. The chromosome contains 853 genes  
encoding a basic set of proteins for DNA replication, transcription,  
translation, solute transport and energy metabolism, but, like Mycoplasma  
genitalium, it contains no genes for cellular biosynthetic reactions.  
Because B. burgdorferi and M. genitalium are distantly related eubacteria,  
we suggest that their limited metabolic capacities reflect convergent  
evolution by gene loss from more metabolically competent progenitors. Of  
430 genes on 11 plasmids, most have no known biological function; 39% of  
plasmid genes are paralogues that form 47 gene families. The biological  
significance of the multiple plasmid-encoded genes is not clear, although  
they may be involved in antigenic variation or immune evasion.

=> e dougherty brian a/au

E1 1 DOUGHERTY BARRY/AU  
E2 11 DOUGHERTY BRIAN/AU  
E3 47 --> DOUGHERTY BRIAN A/AU  
E4 1 DOUGHERTY BRIAN ANDREW/AU  
E5 1 DOUGHERTY BRIAN C/AU  
E6 9 DOUGHERTY BRIAN J/AU  
E7 8 DOUGHERTY BRIAN L/AU  
E8 1 DOUGHERTY BRIAN LYNN/AU  
E9 17 DOUGHERTY BRIAN P/AU  
E10 2 DOUGHERTY BRYAN/AU  
E11 1 DOUGHERTY BRYAN ALVIN/AU  
E12 131 DOUGHERTY C/AU

=> s e2-e4 and borrel?

L7 8 ("DOUGHERTY BRIAN"/AU OR "DOUGHERTY BRIAN A"/AU OR "DOUGHERTY  
BRIAN ANDREW"/AU) AND BORREL?

=> dup rem l7

PROCESSING COMPLETED FOR L7

L8 7 DUP REM L7 (1 DUPLICATE REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 7 ANSWERS - CONTINUE? Y/(N):y

L8 ANSWER 1 OF 7 USPATFULL on STN  
AN 2004:38579 USPATFULL  
TI Streptococcus pneumoniae polynucleotides and sequences  
IN Kunsch, Charles A., Norcross, GA, UNITED STATES  
Choi, Gil H., Rockville, MD, UNITED STATES  
Dillon, Patrick J., Carlsbad, CA, UNITED STATES  
Rosen, Craig A., Laytonsville, MD, UNITED STATES  
Barash, Steven C., Rockville, MD, UNITED STATES  
Fannon, Michael R., Silver Spring, MD, UNITED STATES  
\*\*\*Dougherty, Brian A.\*\*\*, Killingworth, CT, UNITED STATES  
PA Human Genome Sciences, Inc., Rockville, MD, UNITED STATES, 20850 (U.S. corporation)  
PI US 2004029118 A1 20040212  
AI US 2002-158844 A1 20020603 (10)  
RLI Division of Ser. No. US 1997-961527, filed on 30 Oct 1997, GRANTED, Pat. No. US 6420135  
PRAI US 1996-29960P 19961031 (60)  
DT Utility  
FS APPLICATION  
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850  
CLMN Number of Claims: 20  
ECL Exemplary Claim: 1  
DRWN 2 Drawing Page(s)  
LN.CNT 9165  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present invention provides polynucleotide sequences of the genome of Streptococcus pneumoniae, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

L8 ANSWER 2 OF 7 USPATFULL on STN  
AN 2003:148885 USPATFULL  
TI Streptococcus pneumoniae antigens and vaccines  
IN Choi, Gil H., Rockville, MD, United States  
Kunsch, Charles A., Norcross, GA, United States  
Barash, Steven C., Rockville, MD, United States  
Dillon, Patrick J., Carlsbad, CA, United States  
\*\*\*Dougherty, Brian\*\*\*, Killingworth, CT, United States  
Fannon, Michael R., Silver Spring, MD, United States  
Rosen, Craig A., Laytonsville, MD, United States  
PA Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)  
PI US 6573082 B1 20030603  
AI US 2000-536784 20000328 (9)  
RLI Continuation of Ser. No. US 1997-961083, filed on 30 Oct 1997  
PRAI US 1996-29960P 19961031 (60)  
DT Utility  
FS GRANTED  
EXNAM Primary Examiner: Navarro, Mark  
LREP Human Genome Sciences, Inc.  
CLMN Number of Claims: 21  
ECL Exemplary Claim: 1  
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)  
LN.CNT 5072  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and

antibodies in a biological sample.

L8 ANSWER 3 OF 7 USPATFULL on STN  
AN 2002:119562 USPATFULL  
TI Streptococcus pneumoniae antigens and vaccines  
IN Choi, Gil H., Rockville, MD, UNITED STATES  
Kunsch, Charles A., Norcross, GA, UNITED STATES  
Barash, Steven C., Rockville, MD, UNITED STATES  
Dillon, Patrick J., Carlsbad, CA, UNITED STATES  
\*\*\*Dougherty, Brian\*\*\*, Killingworth, CT, UNITED STATES  
Fannon, Michael R., Silver Spring, MD, UNITED STATES  
Rosen, Craig A., Laytonsville, MD, UNITED STATES  
PI US 2002061545 A1 20020523  
AI US 2001-765272 A1 20010122 (9)  
RLI Continuation of Ser. No. US 1997-961083, filed on 30 Oct 1997, UNKNOWN  
DT Utility  
FS APPLICATION  
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850  
CLMN Number of Claims: 21  
ECL Exemplary Claim: 1  
DRWN No Drawings  
LN.CNT 5297  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and antibodies in a biological sample.

L8 ANSWER 4 OF 7 USPATFULL on STN  
AN 2002:55159 USPATFULL  
TI STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES  
IN KUNSCH, CHARLES A., GAITHERSBURG, MD, UNITED STATES  
CHOI, GIL H., ROCKVILLE, MD, UNITED STATES  
DILLON, PATRICK J., CARLSBAD, CA, UNITED STATES  
ROSEN, CRAIG A., LAYTONSVILLE, MD, UNITED STATES  
BARASH, STEVEN C., ROCKVILLE, MD, UNITED STATES  
FANNON, MICHAEL R., SILVER SPRING, MD, UNITED STATES  
\*\*\*DOUGHERTY, BRIAN A.\*\*\*, MT. AIRY, MD, UNITED STATES  
PI US 2002032323 A1 20020314  
US 6420135 B2 20020716  
AI US 1997-961527 A1 19971030 (8)  
PRAI US 1996-29960P 19961031 (60)  
DT Utility  
FS APPLICATION  
LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850  
CLMN Number of Claims: 20  
ECL Exemplary Claim: 1  
DRWN 2 Drawing Page(s)  
LN.CNT 7752  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present invention provides polynucleotide sequences of the genome of Streptococcus pneumoniae, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

L8 ANSWER 5 OF 7 USPATFULL on STN  
AN 2000:167517 USPATFULL  
TI Streptococcus pneumoniae antigens and vaccines  
IN Choi, Gil H., Rockville, MD, United States

Kunsch, Charles A., Atlanta, GA, United States  
Barash, Steven C., Rockville, MD, United States  
Dillon, Patrick J., Carlsbad, CA, United States  
\*\*\*Dougherty, Brian\*\*\*, Killingworth, CT, United States  
Fannon, Michael R., Silver Spring, MD, United States  
Rosen, Craig A., Laytonsville, MD, United States

PA Human Genome Sciences, Inc., Rockville, MD, United States (U.S. corporation)

PI US 6159469 20001212

AI US 1997-961083 19971030 (8)

PRAI US 1996-29960P 19961031 (60)

DT Utility

FS Granted

EXNAM Primary Examiner: Housel, James C.; Assistant Examiner: Hines, Ja-Na A.

LREP Human Genome Sciences, Inc.

CLMN Number of Claims: 73

ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 13121

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention relates to novel vaccines for the prevention or attenuation of infection by Streptococcus pneumoniae. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of Streptococcus pneumoniae. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting Streptococcus nucleic acids, polypeptides and antibodies in a biological sample.

L8 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic fragments and open reading frames

IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; \*\*\*Dougherty, Brian\*\*\*  
\*\*\* A.\*\*\*; Lathigra, Raju; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
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W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

CA 2304925	AA	19981230	CA 1998-2304925	19980618
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AU 9881534	A1	19990104	AU 1998-81534	19980618
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EP 1012157	A1	20000628	EP 1998-931389	19980618
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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRAI US 1997-50359P	P	19970620
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US 1997-53344P	P	19970722
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US 1997-53377P	P	19970722
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US 1997-57483P	P	19970903
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WO 1998-US12764	W	19980618
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AB The present invention provides the complete nucleotide sequence of the \*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide

sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 7 OF 7 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 1

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\*Borrelia\*\*\*  
burgdorferi.

AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun;  
Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen;  
Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle;  
\*\*\*Dougherty, Brian\*\*\*; Tomb, Jean-Francois; Fleischmann, Robert D.;  
Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush,  
John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette;  
Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa;  
Wattney, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl;  
Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts,  
Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.  
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\*Borrelia\*\*\* burgdorferi B31, the  
aetiologic agent of Lyme disease, contains a linear chromosome of 910,725  
base pairs and at least 17 linear and circular plasmids with a combined  
size of more than 533,000 base pairs. The chromosome contains 853 genes  
encoding a basic set of proteins for DNA replication, transcription,  
translation, solute transport and energy metabolism, but, like Mycoplasma  
genitalium, it contains no genes for cellular biosynthetic reactions.  
Because B. burgdorferi and M. genitalium are distantly related eubacteria,  
we suggest that their limited metabolic capacities reflect convergent  
evolution by gene loss from more metabolically competent progenitors. Of  
430 genes on 11 plasmids, most have no known biological function; 39% of  
plasmid genes are paralogues that form 47 gene families. The biological  
significance of the multiple plasmid-encoded genes is not clear, although  
they may be involved in antigenic variation or immune evasion.

=> e lathigra raju/au

E1	112	LATHIGRA R/AU
E2	15	LATHIGRA R B/AU
E3	29	--> LATHIGRA RAJU/AU
E4	2	LATHIGRA RAJU B/AU
E5	1	LATHIGRA RUJU/AU
E6	30	LATHIKA K M/AU
E7	2	LATHIKA KUNNATHATTU M/AU
E8	3	LATHIKA N/AU
E9	2	LATHIKA NAIR/AU
E10	4	LATHIKA P/AU
E11	4	LATHIM D/AU
E12	2	LATHIM DELBERT L/AU

=> s e1-e5 and borrel?

L9 24 ("LATHIGRA R"/AU OR "LATHIGRA R B"/AU OR "LATHIGRA RAJU"/AU OR  
"LATHIGRA RAJU B"/AU OR "LATHIGRA RUJU"/AU) AND BORREL?

=> dup rem l9

PROCESSING COMPLETED FOR L9

L10 6 DUP REM L9 (18 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L10 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN

AN 2000:260328 CAPLUS

DN 132:307239

TI Decorin binding proteins DBP A and B and genes encoding them

IN Hanson, Mark S.; Mullikin, Brian A.; Roberts, William; \*\*\*Lathigra,\*\*\*

\*\*\* Raju\*\*\*

PA Medimmune, Inc., USA

SO PCT Int. Appl., 93 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000021989	A1	20000420	WO 1999-US23481	19991008
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1135409	A1	20010926	EP 1999-954795	19991008
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRAI US 1998-103728P P 19981009

WO 1999-US23481 W 19991008

AB The present invention provides bacterial immunogenic agents for administration to humans and non-human animals to stimulate an immune response. It particularly relates to the vaccination of mammalian species with polypeptides derived from bacterial species that cause Lyme disease as a mechanism for stimulating prodn. of antibodies that protect the vaccine recipient against infection by such pathogenic bacterial species, or make the recipient more resistant to such infection. In another aspect the invention provides antibodies against such proteins and protein complexes that may be used as diagnostics and/or as protective/treatment agents for pathogenic bacterial species.

RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 1

AN 2000:123164 BIOSIS

DN PREV2000000123164

TI A bacterial genome in flux: The twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete \*\*\*Borrelia\*\*\* burgdorferi.

AU Casjens, Sherwood [Reprint author]; Palmer, Nanette; van Vugt, Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; \*\*\*Lathigra, Raju\*\*\*; Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel; Hickey, Erin; Gwinn, Michelle; White, Owen; Fraser, Claire M.

CS Division of Molecular Biology and Genetics, Department of Oncological Sciences, University of Utah Medical School, Salt Lake City, UT, 84132, USA

SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.

CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 5 Apr 2000

Last Updated on STN: 3 Jan 2002

AB We have determined that \*\*\*Borrelia\*\*\* burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside \*\*\*Borrelia\*\*\*, suggesting that they perform specialized functions.

L10 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27959 CAPLUS

DN 130:109198

TI \*\*\*Borrelia\*\*\* polynucleotides and antigenic polypeptides for use as Lyme disease vaccines and diagnostics

IN Choi, Gil H.; Erwin, Alice L.; Hanson, Mark S.; \*\*\*Lathigra, Raju\*\*\*

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 275 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9859071	A1	19981230	WO 1998-US12718	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9881518	A1	19990104	AU 1998-81518	19980618
EP 1009859	A1	20000621	EP 1998-931370	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI US 1997-50359P	P	19970620		
US 1997-53344P	P	19970722		
US 1997-53377P	P	19970722		
US 1997-57483P	P	19970903		
WO 1998-US12718	W	19980618		

AB The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid mols. encoding antigenic polypeptides of \*\*\*Borrelia\*\*\* burgdorferi. Also provided are antigenic polypeptides for use as vaccine and antibodies for diagnosis, as are vectors, host cells and recombinant



methods for producing the same. The invention addnl. relates to diagnostic methods for detecting \*\*\*Borrelia\*\*\* gene expression.  
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic fragments and open reading frames

IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; \*\*\*Lathigra, Raju\*\*\* ; Smith, Hamilton O.

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2304925	AA	19981230	CA 1998-2304925	19980618
AU 9881534	A1	19990104	AU 1998-81534	19980618
EP 1012157	A1	20000628	EP 1998-931389	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI US 1997-50359P	P	19970620		
US 1997-53344P	P	19970722		
US 1997-53377P	P	19970722		
US 1997-57483P	P	19970903		
WO 1998-US12764	W	19980618		

AB The present invention provides the complete nucleotide sequence of the \*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 2

AN 1998:510282 BIOSIS

DN PREV199800510282

TI Molecular analysis of sequence heterogeneity among genes encoding decorin binding proteins A and B of \*\*\*Borrelia\*\*\* burgdorferi sensu lato.

AU Roberts, William C.; Mullikin, Brian A.; \*\*\*Lathigra, Raju\*\*\* ; Hanson, Mark S. [Reprint author]

CS MedImmune Inc., 35 West Watkins Mill Road, Gaithersburg, MD 20878, USA

SO Infection and Immunity, (Nov., 1998) Vol. 66, No. 11, pp. 5275-5285.  
print.

CODEN: INFIBR. ISSN: 0019-9567.

DT Article

LA English

ED Entered STN: 18 Dec 1998

Last Updated on STN: 18 Dec 1998

AB Immunization of mice with \*\*\**Borrelia*\*\*\* burgdorferi decorin binding protein A (DbpA), one of two gene products of the dbpBA locus, has been shown recently to confer protection against challenge. Hyperimmune DbpA antiserum killed a large number of *B. burgdorferi* sensu lato isolates of diverse phylogeny and origin, suggesting conservation of the protective epitope(s). In order to evaluate the heterogeneity of DbpA and DbpB and to facilitate defining the conserved epitope(s) of these antigens, the sequences of the dbpA genes from 29 *B. burgdorferi* sensu lato isolates and of the dbpB genes from 15 *B. burgdorferi* sensu lato isolates were determined. The predicted DbpA sequences were fairly heterogeneous among the isolates (58.3 to 100% similarity), but DbpA sequences with the highest similarity tended to group into species previously defined by well-characterized chromosomal markers. In contrast, the predicted DbpB sequences were highly conserved (96.3 to 100% similarity). Substantial diversity in DbpA sequence was seen among isolates previously shown to be killed by antiserum against a single DbpA, suggesting that one or more conserved protective epitopes are composed of noncontiguous amino acids. The observation of individual dbpA alleles with sequence elements characteristic of more than one *B. burgdorferi* sensu lato species was consistent with a role for genetic recombination in the generation of dbpA diversity.

L10 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 3

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\**Borrelia*\*\*\* burgdorferi.

AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; \*\*\*Lathigra, Raju\*\*\*; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.

CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\**Borrelia*\*\*\* burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like *Mycoplasma genitalium*, it contains no genes for cellular biosynthetic reactions. Because *B. burgdorferi* and *M. genitalium* are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e smith hamilton o/au

E1 1 SMITH HALLAM C/AU  
 E2 56 SMITH HAMILTON/AU  
 E3 164 --> SMITH HAMILTON O/AU  
 E4 4 SMITH HAMILTON OTHANEL/AU  
 E5 39 SMITH HAMISH R C/AU  
 E6 3 SMITH HAMMOND C/AU  
 E7 7 SMITH HAMMOND C A/AU  
 E8 2 SMITH HAMMOND CAROL A/AU  
 E9 1 SMITH HAMPTON/AU  
 E10 2 SMITH HAMPTON D/AU  
 E11 11 SMITH HAMPTON D JR/AU  
 E12 1 SMITH HAMPTON DAVID JR/AU

=> s e2-e4 and borrel?

L11 8 ("SMITH HAMILTON"/AU OR "SMITH HAMILTON O"/AU OR "SMITH HAMILTON OTHANEL"/AU) AND BORREL?

=> dup rem l11

PROCESSING COMPLETED FOR L11

L12 6 DUP REM L11 (2 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 6 ANSWERS - CONTINUE? Y/(N):y

L12 ANSWER 1 OF 6 USPATFULL on STN

AN 2003:244254 USPATFULL

TI Nucleotide sequence of the Mycoplasma genitalium genome, fragments thereof, and uses thereof

IN Fraser, Claire M., Potomac, MD, UNITED STATES

Adams, Mark D., Rockville, MD, UNITED STATES

Gocayne, Jeannine D., Potomac, MD, UNITED STATES

Hutchison, Clyde A., III, Chapel Hill, MD, UNITED STATES

\*\*\*Smith, Hamilton O.\*\*\*, Reisterstown, MD, UNITED STATES

Venter, J. Craig, Queenstown, MD, UNITED STATES

White, Owen R., Rockville, MD, UNITED STATES

PA Johns Hopkins University, Baltimore, MD (U.S. corporation)

PI US 2003170663 A1 20030911

AI US 2002-205220 A1 20020726 (10)

RLI Division of Ser. No. US 1995-545528, filed on 19 Oct 1995, PENDING  
 Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995,  
 PENDING Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun  
 1995, ABANDONED

DT Utility

FS APPLICATION

LREP HUMAN GENOME SCIENCES INC, 9410 KEY WEST AVENUE, ROCKVILLE, MD, 20850

CLMN Number of Claims: 19

ECL Exemplary Claim: 1

DRWN 23 Drawing Page(s)

LN.CNT 6270

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO: 1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L12 ANSWER 2 OF 6 USPATFULL on STN

AN 2003:81597 USPATFULL

TI Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof

IN Fraser, Claire M., Potomac, MD, United States

Adams, Mark D., N. Potomac, MD, United States

Gocayne, Jeannine D., Silver Spring, MD, United States  
Hutchison, III, Clyde A., Chapel Hill, NC, United States  
\*\*\*Smith, Hamilton O.\*\*\*, Towson, MD, United States  
Venter, J. Craig, Potomac, MD, United States  
White, Owen, Gaithersburg, MD, United States  
PA The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)  
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)  
The University of North Carolina at Chapel Hill, Chapel Hill, NC, United States (U.S. corporation)  
PI US 6537773 B1 20030325  
AI US 1995-545528 19951019 (8)  
RLI Continuation-in-part of Ser. No. US 1995-488018, filed on 7 Jun 1995, now abandoned Continuation-in-part of Ser. No. US 1995-473545, filed on 7 Jun 1995, now abandoned  
DT Utility  
FS GRANTED  
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard  
LREP Human Genome Sciences, Inc.  
CLMN Number of Claims: 44  
ECL Exemplary Claim: 1  
DRWN 23 Drawing Figure(s); 23 Drawing Page(s)  
LN.CNT 15190  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present invention provides the nucleotide sequence of the entire genome of Mycoplasma genitalium, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the Mycoplasma genitalium genome.

L12 ANSWER 3 OF 6 USPATFULL on STN  
AN 2003:6806 USPATFULL  
TI Selected polynucleotide and polypeptide sequences of the methanogenic archaeon, methanococcus jannashii  
IN Bult, Carol J., Bar Harbor, ME, United States  
White, Owen R., Gaithersburg, MD, United States  
\*\*\*Smith, Hamilton O.\*\*\*, Baltimore, MD, United States  
Woese, Carl R., Urbana, IL, United States  
Venter, J. Craig, Rockville, MD, United States  
PA The Board of Trustees of the University of Illinois, Urbana, IL, United States (U.S. corporation)  
The Institute for Genomic Research, Rockville, MD, United States (U.S. corporation)  
Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)  
PI US 6503729 B1 20030107  
AI US 1997-916421 19970822 (8)  
PRAI US 1996-24428P 19960822 (60)  
DT Utility  
FS GRANTED  
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Schnizer, Richard  
LREP Human Genome Sciences, Inc.  
CLMN Number of Claims: 107  
ECL Exemplary Claim: 1  
DRWN 2 Drawing Figure(s); 2 Drawing Page(s)  
LN.CNT 4244  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
AB The present application describes selected polynucleotide sequence from the 1.66-megabase pair genome sequence of an autotrophic archaeon, Methanococcus jannaschii, and its 58- and 16-kilobase pair extrachromosomal elements.

L12 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:27841 CAPLUS

DN 130:62074

TI Nucleotide sequence of \*\*\*Borrelia\*\*\* burgdorferi genome and genomic fragments and open reading frames

IN Fraser, Claire; White, Owen R.; Clayton, Rebecca; Dougherty, Brian A.; Lathigra, Raju; \*\*\*Smith, Hamilton O.\*\*\*

PA Human Genome Sciences, Inc., USA; Medimmune, Inc.

SO PCT Int. Appl., 1128 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI WO 9858943	A1	19981230	WO 1998-US12764	19980618
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W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

CA 2304925	AA	19981230	CA 1998-2304925	19980618
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AU 9881534	A1	19990104	AU 1998-81534	19980618
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EP 1012157	A1	20000628	EP 1998-931389	19980618
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R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRAI US 1997-50359P	P	19970620
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US 1997-53344P	P	19970722
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US 1997-53377P	P	19970722
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US 1997-57483P	P	19970903
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WO 1998-US12764	W	19980618
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AB The present invention provides the complete nucleotide sequence of the \*\*\*Borrelia\*\*\* burgdorferi chromosome and 154 contigs representing the majority of the sequence of the B. burgdorferi extrachromosomal elements. Also provided are polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. Each open reading frame is identified with a function by homol. to a known gene or polypeptide. The present invention further demonstrates that a large sequence can be sequenced using a random approach, eliminating the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 1

AN 1998:361763 BIOSIS

DN PREV199800361763

TI Complete genome sequence of Treponema pallidum, the syphilis spirochete.

AU Fraser, Claire M. [Reprint author]; Norris, Steven J.; Weinstock, George M.; White, Owen; Sutton, Granger G.; Dodson, Robert; Gwinn, Michelle; Hickey, Erin K.; Clayton, Rebecca; Ketchum, Karen A.; Sodergren, Erica; Hardham, John M.; McLeod, Michael P.; Salzberg, Steven; Peterson, Jeremy; Khalak, Hanif; Richardson, Delwood; Howell, Jerrilyn K.; Chidambaram, Monjula; Utterback, Teresa; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Cotton, Matthew D.; Fujii, Claire; Garland, Stacey; Hatch, Bonnie; Horst, Kurt; Roberts, Kevin; Sandusky, Mina; Weidman, Janice; \*\*\*Smith,\*\*\*  
\*\*\* Hamilton O.\*\*\* ; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Science (Washington D C), (July 17, 1998) Vol. 281, No. 5375, pp. 375-388.

print.

CODEN: SCIEAS. ISSN: 0036-8075.

DT Article

LA English

ED Entered STN: 27 Aug 1998

Last Updated on STN: 27 Aug 1998

AB The complete genome sequence of *Treponema pallidum* was determined and shown to be 1,138,006 base pairs containing 1041 predicted coding sequences (open reading frames). Systems for DNA replication, transcription, translation, and repair are intact, but catabolic and biosynthetic activities are minimized. The number of identifiable transporters is small, and no phosphoenolpyruvate: phosphotransferase carbohydrate transporters were found. Potential virulence factors include a family of 12 potential membrane proteins and several putative hemolysins. Comparison of the *T. pallidum* genome sequence with that of another pathogenic spirochete, \*\*\**Borrelia*\*\*\* burgdorferi, the agent of Lyme disease, identified unique and common genes and substantiates the considerable diversity observed among pathogenic spirochetes.

L12 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 2

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\**Borrelia*\*\*\* burgdorferi.

AU Fraser, Claire M. [Reprint author]; Casjens, Sherwood; Huang, Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White, Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle; Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson, Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John; Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams, Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Wattney, Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey; Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch, Bonnie; \*\*\*Smith, Hamilton O.\*\*\*; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.

CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\**Borrelia*\*\*\* burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like *Mycoplasma genitalium*, it contains no genes for cellular biosynthetic reactions. Because *B. burgdorferi* and *M. genitalium* are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

=> e casjens sherwood/au

E1 53 CASJENS S R/AU

E2 1 CASJENS SH/AU

E3 116 --> CASJENS SHERWOOD/AU

E4 19 CASJENS SHERWOOD R/AU

E5 1 CASJENS SHERWOOD REID/AU

E6 4 CASJKA C/AU

E7 3 CASJKA CHANTAL/AU

E8 2 CASKA B/AU

E9 2 CASKA B A/AU  
E10 2 CASKA BARBARA/AU  
E11 3 CASKA JOSEF/AU  
E12 4 CASKADON M A/AU

=> s e1-e5 and borrel?

L13 46 ("CASJENS S R"/AU OR "CASJENS SH"/AU OR "CASJENS SHERWOOD"/AU  
OR "CASJENS SHERWOOD R"/AU OR "CASJENS SHERWOOD REID"/AU) AND  
BORREL?

=> dup rem l13

PROCESSING COMPLETED FOR L13

L14 26 DUP REM L13 (20 DUPLICATES REMOVED)

=> d bib ab 1-

YOU HAVE REQUESTED DATA FROM 26 ANSWERS - CONTINUE? Y/(N):y

L14 ANSWER 1 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

AN 2004:527503 CAPLUS

TI Telomere exchange between linear replicons of \*\*\*Borrelia\*\*\*  
burgdorferi

AU Huang, Wai Mun; Robertson, Margaret; Aron, John; \*\*\*Casjens, Sherwood\*\*\*  
CS Department of Pathology, University of Utah Medical School, Salt Lake  
City, UT, 84132, USA

SO Journal of Bacteriology (2004), 186(13), 4134-4141  
CODEN: JOBAAY; ISSN: 0021-9193

PB American Society for Microbiology

DT Journal

LA English

AB Spirochetes in the genus \*\*\*Borrelia\*\*\* carry a linear chromosome and  
numerous linear plasmids that have covalently closed hairpin telomeres.  
The overall organization of the large chromosome of \*\*\*Borrelia\*\*\*  
burgdorferi appears to have been quite stable over recent evolutionary  
time; however, a large fraction of natural isolates carry differing  
lengths of DNA that extend the right end of the chromosome between about 7  
and 20 kbp relative to the shortest chromosomes. We present evidence here  
that a rather recent nonhomologous recombination event in the B.  
burgdorferi strain Sh-2-82 lineage has replaced its right chromosomal  
telomere with a large portion of the linear plasmid lp21, which is present  
in the strain B31 lineage. At least two successive rounds of addn. of  
linear plasmid genetic material to the chromosomal right end appear to  
have occurred at the Sh-2-82 right telomere, suggesting that this is an  
evolutionary mechanism by which plasmid genetic material can become part  
of the chromosome. The unusual nonhomologous nature of this rearrangement  
suggests that, barring horizontal transfer, it can be used as a unique  
genetic marker for this lineage of B. burgdorferi chromosomes.

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 2 OF 26 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

AN 2003:1039719 SCISEARCH

GA The Genuine Article (R) Number: 743TX

TI Bidirectional replication from an internal ori site of the linear N15  
plasmid prophage

AU Ravin N V (Reprint); Kuprianov V V; Gilcrease E B; \*\*\*Casjens S R\*\*\*

CS Russian Acad Sci, Ctr Bioengn, Prosp 60 Let Oktiabria, Bldg 7-1, Moscow  
117312, Russia (Reprint); Russian Acad Sci, Ctr Bioengn, Moscow 117312,  
Russia; Univ Utah, Sch Med, Dept Pathol, Salt Lake City, UT 84132 USA

CYA Russia; USA

SO NUCLEIC ACIDS RESEARCH, (15 NOV 2003) Vol. 31, No. 22, pp. 6552-6560.

Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.

ISSN: 0305-1048.

DT Article; Journal

LA English

REC Reference Count: 52

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB The prophage of coliphage N15 is not integrated into the chromosome but exists as a linear plasmid molecule with covalently closed hairpin ends (telomeres). Upon infection the injected phage DNA circularizes via its cohesive ends. Then, a phage-encoded enzyme, protelomerase, cuts the circle and forms the hairpin telomeres. N15 protelomerase acts as a telomere-resolving enzyme during prophage DNA replication. We characterized the N15 replicon and found that replication of circular N15 miniplasmids requires only the repA gene, which encodes a multidomain protein homologous to replication proteins of bacterial plasmids replicated by a theta-mechanism. Replication of a linear N15 miniplasmid also requires the protelomerase gene and telomere regions. N15 prophage replication is initiated at an internal ori site located within repA and proceeds bidirectionally. Electron microscopy data suggest that after duplication of the left telomere, protelomerase cuts this site generating Y-shaped molecules. Full replication of the molecule and subsequent resolution of the right telomere then results in two linear plasmid molecules. N15 prophage replication thus appears to follow a mechanism that is distinct from that employed by eukaryotic replicons with this type of telomere and suggests the possibility of evolutionarily independent appearances of prokaryotic and eukaryotic replicons with covalently closed telomeres.

L14 ANSWER 3 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 2

AN 2003:223631 BIOSIS

DN PREV200300223631

TI Profiling of temperature-induced changes in \*\*\*Borrelia\*\*\* burgdorferi gene expression by using whole genome arrays.

AU Ojaimi, Caroline; Brooks, Chad; \*\*\*Casjens, Sherwood\*\*\* ; Rosa, Patricia; Elias, Abdallah; Barbour, Alan; Jasinskas, Algis; Benach, Jorge; Katona, Laura; Radolf, Justin; Caimano, Melissa; Skare, Jon; Swingle, Kristen; Akins, Darin; Schwartz, Ira [Reprint Author]

CS Department of Microbiology and Immunology, New York Medical College, Valhalla, NY, 10595, USA  
darrin-akins@ouhsc.edu; Schwartz@nymc.edu

SO Infection and Immunity, (April 2003) Vol. 71, No. 4, pp. 1689-1705. print.  
ISSN: 0019-9567 (ISSN print).

DT Article

LA English

ED Entered STN: 7 May 2003

Last Updated on STN: 7 May 2003

AB \*\*\*Borrelia\*\*\* burgdorferi is the etiologic agent of Lyme disease, the most prevalent arthropod-borne disease in the United States. The genome of the type strain, B31, consists of a 910,725-bp linear chromosome and 21 linear and circular plasmids comprising 610,694 bp. During its life cycle, the spirochete exists in distinctly different environments, cycling between a tick vector and a mammalian host. Temperature is one environmental factor known to affect B. burgdorferi gene expression. To identify temperature-responsive genes, genome arrays containing 1,662 putative B. burgdorferi open reading frames (ORFs) were prepared on nylon membranes and employed to assess gene expression in B. burgdorferi B31 grown at 23 and 35degreeC. Differences in expression of more than 3.5 orders of magnitude could be readily discerned and quantitated. At least minimal expression from 91% of the arrayed ORFs could be detected. A total of 215 ORFs were differentially expressed at the two temperatures; 133 were expressed at significantly greater levels at 35degreeC, and 82 were more significantly expressed at 23degreeC. Of these 215 ORFs, 134 are characterized as genes of unknown function. One hundred thirty-six (63%) of the differentially expressed genes are plasmid encoded. Of particular interest is plasmid lp54 which contains 76 annotated putative genes; 31 of these exhibit temperature-regulated expression. These findings underscore the important role plasmid-encoded genes may play in adjustment of B. burgdorferi to growth under diverse environmental conditions.

L14 ANSWER 4 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

AN 2003:101209 CAPLUS



DN 138:349177  
TI \*\*\*Borrelia\*\*\* burgdorferi gene expression profiling with  
membrane-based arrays  
AU Ojaimi, Caroline; Brooks, Chad; Akins, Darrin; \*\*\*Casjens, Sherwood\*\*\*  
; Rosa, Patricia; Elias, Abdallah; Barbour, Alan; Jasinskas, Algis;  
Benach, Jorge; Katonah, Laura; Radolf, Justin; Caimano, Melissa; Skare,  
Jon; Swingle, Kristen; Sims, Simon; Schwartz, Ira  
CS Department of Microbiology and Immunology, New York Medical College,  
Valhalla, NY, 10595, USA  
SO Methods in Enzymology (2002), 358(Bacterial Pathogenesis, Part C), 165-177  
CODEN: MENZAU; ISSN: 0076-6879  
PB Elsevier Science  
DT Journal  
LA English  
AB A method to study \*\*\*Borrelia\*\*\* burgdorferi gene expression profiling  
with membrane-based arrays is described. Specifically, the methods  
contains prepn. of PCR-amplified open reading frames from B. burgdorferi  
strain B31 MI, the strain whose genome sequence has been elucidated,  
synthesis of labeled cDNA hybridization probe, hybridization, and  
statistical anal. about the obtained data.  
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 5 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:554148 BIOSIS  
DN PREV200100554148  
TI Bacteriophages of \*\*\*Borrelia\*\*\* burgdorferi and other spirochetes.  
AU Eggers, Christian H. [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ;  
Samuels, D. Scott  
CS Center for Microbial Pathogenesis, University of Connecticut Health  
Center, Farmington, CT, 06030, USA  
SO Saier, Milton H., Jr. [Editor]; Garcia-Lara, Jorge [Editor]. (2001) pp.  
35-44. JMMB Symposium Series. The spirochetes: Molecular and cellular  
biology. print.  
Publisher: Horizon Scientific Press, 32 Hewitts Lane, Wymondham, Norfolk,  
NR18 0JA, UK. Series: JMMB Symposium Series.  
ISBN: 1-898486-27-1 (cloth).  
DT Book  
Book; (Book Chapter)  
LA English  
ED Entered STN: 28 Nov 2001  
Last Updated on STN: 25 Feb 2002

L14 ANSWER 6 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
AN 2001:553349 BIOSIS  
DN PREV200100553349  
TI \*\*\*Borrelia\*\*\* genomes.  
AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]  
CS Department of of Oncological Sciences, Division of Molecular Biology and  
Genetics, University of Utah, Salt Lake City, UT, 84132, USA  
SO Saier, Milton H., Jr. [Editor]; Garcia-Lara, Jorge [Editor]. (2001) pp.  
75-85. JMMB Symposium Series. The spirochetes: Molecular and cellular  
biology. print.  
Publisher: Horizon Scientific Press, 32 Hewitts Lane, Wymondham, Norfolk,  
NR18 0JA, UK. Series: JMMB Symposium Series.  
ISBN: 1-898486-27-1 (cloth).  
DT Book  
Book; (Book Chapter)  
LA English  
ED Entered STN: 28 Nov 2001  
Last Updated on STN: 25 Feb 2002

L14 ANSWER 7 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 4  
AN 2000:504125 BIOSIS  
DN PREV200000504125  
TI A second allele of eppA in \*\*\*Borrelia\*\*\* burgdorferi strain B31 is

located on the previously undetected circular plasmid cp9-2.

AU Miller, Jennifer C.; Bono, James L.; Babb, Kelly; El-Hage, Nazira;  
\*\*\*Casjens, Sherwood\*\*\* ; Stevenson, Brian [Reprint author]  
CS Department of Microbiology and Immunology, University of Kentucky College  
of Medicine, Lexington, KY, 40536-0298, USA  
SO Journal of Bacteriology, (November, 2000) Vol. 182, No. 21, pp. 6254-6258.  
print.  
CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

OS Genbank-AF213472

ED Entered STN: 22 Nov 2000

Last Updated on STN: 12 Feb 2002

AB Although sequence analysis of \*\*\*Borrelia\*\*\* burgdorferi isolate B31  
was recently declared "complete," we found that cultures of this strain  
can contain a novel 9-kb circular plasmid, cp9-2. The newly described  
plasmid contains both sequence similarities with and differences from the  
previously identified B31 plasmid cp9-1 (formerly cp9). cp9-1 and cp9-2  
each encode a unique allele of EppA, a putative membrane protein  
synthesized by B. burgdorferi during mammalian infection.

L14 ANSWER 8 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 5

AN 2000:254050 BIOSIS

DN PREV200000254050

TI Distribution of twelve linear extrachromosomal DNAs in natural isolates of  
lyme disease spirochetes.

AU Palmer, Nanette; Fraser, Claire; \*\*\*Casjens, Sherwood\*\*\* [Reprint  
author]

CS Department of Oncological Sciences, University of Utah Medical School,  
Salt Lake City, UT, 84132, USA

SO Journal of Bacteriology, (May, 2000) Vol. 182, No. 9, pp. 2476-2480.  
print.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 21 Jun 2000

Last Updated on STN: 5 Jan 2002

AB We have analyzed a panel of independent North American isolates of the  
Lyme disease agent spirochete, \*\*\*Borrelia\*\*\* burgdorferi (sensu  
stricto), for the presence of linear plasmids with sequence similarities  
to the 12 linear plasmids present in the B. burgdorferi type strain,  
isolate B31. The frequency of similarities to probes from each of the 12  
B31 plasmids varied from 13 to 100% in the strain panel examined, and  
these similarities usually reside on plasmids similar in size to the  
cognate B31 plasmid. Sequences similar to 5 of the 12 B31 plasmids were  
found in all of the isolates examined, and >66% of the panel members  
hybridized to probes from 4 other plasmids. Sequences similar to most of  
the B. burgdorferi B31 plasmid-derived DNA probes used were also found on  
linear plasmids in the related Eurasian Lyme agents \*\*\*Borrelia\*\*\*  
garinii and \*\*\*Borrelia\*\*\* afzelii; however, some of these plasmids  
had uniform but substantially different sizes from their B. burgdorferi  
counterparts.

L14 ANSWER 9 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 6

AN 2000:123164 BIOSIS

DN PREV200000123164

TI A bacterial genome in flux: The twelve linear and nine circular  
extrachromosomal DNAs in an infectious isolate of the Lyme disease  
spirochete \*\*\*Borrelia\*\*\* burgdorferi.

AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]; Palmer, Nanette; van Vugt,  
Rene; Huang, Wai Mun; Stevenson, Brian; Rosa, Patricia; Lathigra, Raju;  
Sutton, Granger; Peterson, Jeremy; Dodson, Robert J.; Haft, Daniel;  
Hickey, Erin; Gwinn, Michelle; White, Owen; Fraser, Claire M.

CS Division of Molecular Biology and Genetics, Department of Oncological  
Sciences, University of Utah Medical School, Salt Lake City, UT, 84132,

USA

SO Molecular Microbiology, (Feb., 2000) Vol. 35, No. 3, pp. 490-516. print.  
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 5 Apr 2000

Last Updated on STN: 3 Jan 2002

AB We have determined that \*\*\*Borrelia\*\*\* burgdorferi strain B31 MI carries 21 extrachromosomal DNA elements, the largest number known for any bacterium. Among these are 12 linear and nine circular plasmids, whose sequences total 610 694 bp. We report here the nucleotide sequence of three linear and seven circular plasmids (comprising 290 546 bp) in this infectious isolate. This completes the genome sequencing project for this organism; its genome size is 1 521 419 bp (plus about 2000 bp of undetermined telomeric sequences). Analysis of the sequence implies that there has been extensive and sometimes rather recent DNA rearrangement among a number of the linear plasmids. Many of these events appear to have been mediated by recombinational processes that formed duplications. These many regions of similarity are reflected in the fact that most plasmid genes are members of one of the genome's 161 paralogous gene families; 107 of these gene families, which vary in size from two to 41 members, contain at least one plasmid gene. These rearrangements appear to have contributed to a surprisingly large number of apparently non-functional pseudogenes, a very unusual feature for a prokaryotic genome. The presence of these damaged genes suggests that some of the plasmids may be in a period of rapid evolution. The sequence predicts 535 plasmid genes gtoreq300 bp in length that may be intact and 167 apparently mutationally damaged and/or unexpressed genes (pseudogenes). The large majority, over 90%, of genes on these plasmids have no convincing similarity to genes outside \*\*\*Borrelia\*\*\*, suggesting that they perform specialized functions.

L14 ANSWER 10 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 7

AN 2002:140399 BIOSIS

DN PREV200200140399

TI The role of genomics in approaching the study of \*\*\*Borrelia\*\*\* DNA replication.

AU Garcia-Lara, Jorge [Reprint author]; Picardeau, Mathieu; Hinnebusch, B. Joseph; Huang, Wai Mun; \*\*\*Casjens, Sherwood\*\*\*

CS Department of Microbiology, University of Georgia, 546 Biological Sciences Building, Athens, GA, 30602, USA  
jgarcial@panda.uchc.edu

SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol. 2, No. 4, pp. 447-454. print.  
ISSN: 1464-1801.

DT Article

General Review; (Literature Review)

LA English

ED Entered STN: 6 Feb 2002

Last Updated on STN: 26 Feb 2002

AB The identification of chromosomal and episomal origins of replication in the genome of the causative agent of Lyme disease, the spirochete \*\*\*Borrelia\*\*\* burgdorferi, has been greatly facilitated by genomics. Analysis of genome features, including strand compositional asymmetries, organizational similarities to other bacterial origins of replication, and the presence of homologues of genes involved in replication and partitioning, have contributed to the identification of a collection of putative origins of replication within the \*\*\*Borrelia\*\*\* genome. This analysis has provided the basis for the experimental verification of origins in the linear chromosome and in the linear plasmid lp28-2. Information generated during the study of these origins will significantly contribute to the understanding of the mechanisms of replication and partitioning in \*\*\*Borrelia\*\*\*.

L14 ANSWER 11 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 8

AN 2002:140393 BIOSIS  
 DN PREV200200140393  
 TI \*\*\*Borrelia\*\*\* genomes in the year 2000.  
 AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]  
 CS Department of Oncological Sciences, University of Utah Medical School,  
 Salt Lake City, UT, 84132, USA  
 sherwood.casjens@hci.utah.edu  
 SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol.  
 2, No. 4, pp. 401-410. print.  
 ISSN: 1464-1801.  
 DT Article  
 General Review; (Literature Review)  
 LA English  
 ED Entered STN: 6 Feb 2002  
 Last Updated on STN: 26 Feb 2002  
 AB All analyzed members of the spirochete genus \*\*\*Borrelia\*\*\* contain a  
 linear chromosome about 910 kbp long. The complete sequence of the B.  
 burgdorferi B31 genome predicts that its chromosome carries essentially  
 all of this organism's housekeeping genes. In accordance with these  
 bacterial species' obligatory parasitic lifestyle, its genes encode  
 enzymes that are capable of only a minimal metabolism, in which all  
 nucleotides, amino acids, fatty acids and enzyme cofactors must be  
 scavenged from the host. In addition to the chromosome, all  
 \*\*\*Borrelia\*\*\* isolates examined carry multiple linear and circular  
 plasmids with lengths between 5 and 200 kbp. The plasmids, which account  
 for over 600 kbp in isolate B31, carry very few genes with homology to  
 genes outside of the \*\*\*Borrelia\*\*\* genus. But they do carry numerous  
 predicted lipoprotein genes, many of which have been shown to be or  
 are expected to be outer surface proteins. Ten of the linear plasmids  
 have strikingly low protein coding potential for bacterial DNA. These  
 plasmids have enjoyed numerous past duplicative rearrangements, which have  
 resulted in the presence of a substantial fraction of the DNA that appears  
 to be currently undergoing mutational decay, presumably because it is no  
 longer under selection for function.

L14 ANSWER 12 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 DUPLICATE 9

AN 2002:140388 BIOSIS  
 DN PREV200200140388  
 TI Bacteriophages of spirochetes.  
 AU Eggers, Christian H.; \*\*\*Casjens, Sherwood\*\*\* ; Hayes, Stanley F.;  
 Garon, Claude F.; Damman, Christopher J.; Oliver, Donald B.; Samuels, D.  
 Scott [Reprint author]  
 CS Division of Biological Sciences, University of Montana, Missoula, MT,  
 59812, USA  
 samuels@selway.umt.edu  
 SO Journal of Molecular Microbiology and Biotechnology, (October, 2000) Vol.  
 2, No. 4, pp. 365-373. print.  
 ISSN: 1464-1801.  
 DT Article  
 General Review; (Literature Review)  
 LA English  
 ED Entered STN: 6 Feb 2002  
 Last Updated on STN: 26 Feb 2002  
 AB Historically, a number of bacteriophage-like particles have been observed  
 in association with members of the bacterial order Spirochetales, the  
 spirochetes. In the last decade, several spirochete bacteriophages have  
 been isolated and characterized at the molecular level. We have recently  
 characterized a bacteriophage of the Lyme disease agent, \*\*\*Borrelia\*\*\*  
 burgdorferi, which we have designated variant phiBB-1. Here we review the  
 history of the association between the spirochetes and their  
 bacteriophages, with a particular emphasis on variant phiBB-1 and its  
 prophage, the 32-kb circular plasmid family of B. burgdorferi.

L14 ANSWER 13 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
 AN 2001:63185 BIOSIS  
 DN PREV200100063185

TI The unusual linear plasmids of the Lyme disease spirochete  
\*\*\*borrelia\*\*\* burgdorferi.  
AU \*\*\*Casjens, S. R.\*\*\* [Reprint author]  
CS Dept. of Oncological Sciences, U. of Utah Medical School, Salt Lake City,  
UT, 84132, USA  
SO Biochemical Society Transactions, (October, 2000) Vol. 28, No. 5, pp.  
A102. print.  
Meeting Info.: 18th International Congress of Biochemistry and Molecular  
Biology. Birmingham, UK. July 16-20, 2000. International Union of  
Biochemistry and Molecular Biology; Federation of European Biochemical  
Societies; Biochemical Society.  
CODEN: BCSTB5. ISSN: 0300-5127.  
DT Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LA English  
ED Entered STN: 31 Jan 2001  
Last Updated on STN: 12 Feb 2002

L14 ANSWER 14 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN

AN 1999:734795 CAPLUS

DN 132:90395

TI Evolution of the linear DNA replicons of the \*\*\*Borrelia\*\*\*  
spirochetes

AU \*\*\*Casjens, Sherwood\*\*\*

CS Division of Molecular Biology and Genetics, Department of Oncological,  
University of Utah Medical School, Salt Lake City, UT, 84321, USA

SO Current Opinion in Microbiology (1999), 2(5), 529-534

CODEN: COMIF7; ISSN: 1369-5274

PB Current Biology Publications

DT Journal; General Review

LA English

AB A review with 59 refs. Members of the spirochete genus \*\*\*Borrelia\*\*\*  
carry numerous linear DNA replicons with covalently closed hairpin  
telomeres. The genome of one member of this genus, B. burgdorferi B31,  
has now been completely characterized and contains a linear chromosome,  
twelve linear plasmids and nine circular extra-chromosomal elements. The  
phylogenetic position of the \*\*\*Borrelia\*\*\* spirochetes strongly  
suggests that a progenitor with circular replicons acquired the ability to  
replicate linear DNA mols.

RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 15 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

AN 1998:412591 BIOSIS

DN PREV199800412591

TI \*\*\*Borrelia\*\*\* burgdorferi and the other Lyme disease spirochetes.

AU \*\*\*Casjens, Sherwood\*\*\* ; Huang, Wai Mun

CS Dep. Oncol. Sci., Div. Mol. Biol. and Genet., Univ. Utah Health Sci.  
Cent., Salt Lake City, UT 84132, USA

SO de Bruijn, F. J. [Editor]; Lupski, J. R. [Editor]; Weinstock, G. M.  
[Editor]. (1998) pp. 621-624. Bacterial genomes: Physical structure and  
analysis. print.

Publisher: Chapman and Hall, Inc., 29 West 35th Street, New York, New  
York, USA; Chapman and Hall Ltd., 2-6 Boundary Row, London SE1 8HN,  
England.

ISBN: 0-412-99141-1.

DT Book

Book; (Book Chapter)

LA English

ED Entered STN: 2 Oct 1998

Last Updated on STN: 2 Oct 1998

L14 ANSWER 16 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 10

AN 1998:391139 BIOSIS

DN PREV199800391139

TI Evidence of past recombination events among the genes encoding the Erp

antigens of \*\*\*Borrelia\*\*\* burgdorferi.  
AU Stevenson, Brian [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ; Rosa, Patricia  
CS Dep. Microbiol. Immunol., MS 415 UKMC, Univ. Kentucky, Lexington, KY 40536, USA  
SO Microbiology (Reading), (July, 1998) Vol. 144, No. 7, pp. 1869-1879. print.  
ISSN: 1350-0872.  
DT Article  
LA English  
OS Genbank-AF022479; Genbank-AF022480; Genbank-AF022481; Genbank-AF022482; Genbank-AF022483  
ED Entered STN: 10 Sep 1998  
Last Updated on STN: 10 Sep 1998  
AB A single \*\*\*Borrelia\*\*\* burgdorferi bacterium may contain six or more different 32 kb circular plasmids (cp32s). Although these plasmids are homologous throughout much of their sequences, two loci have been identified at which they can vary significantly. The cp32 plasmids and their relatives each contain two adjacent genes, orfC and orf3, that vary in sequence between plasmids found within clones of individual bacteria. The orfC gene product is homologous to proteins involved in partitioning of bacterial plasmids, and the differences at this locus between plasmids may account for their compatibility. The orfC-orf3 loci are located approximately 5 kb from another variable locus called erp. The orfC-orf3 loci were used as physically linked markers to assess genetic rearrangements in the erp loci; this revealed examples of recombination involving both individual genes and entire erp loci. Recombination of the genes encoding the Erp antigens might contribute to the evasion of the mammalian immune response and could play roles in the establishment and persistence of B. burgdorferi infections in mammalian hosts.

L14 ANSWER 17 OF 26 CAPLUS COPYRIGHT 2004 ACS on STN  
AN 1997:778273 CAPLUS  
DN 128:71459  
TI \*\*\*Borrelia\*\*\* burgdorferi and the other Lyme disease spirochetes  
AU \*\*\*Casjens, Sherwood\*\*\* ; Huang, Wai Mun  
CS Department of Oncological Sciences Division of Molecular Biology & Genetics, University of Utah Health Science Center, Salt Lake City, UT, 84132, USA  
SO Bacterial Genomes (1998), 621-624. Editor(s): De Bruijn, Frans J.; Lupski, James R.; Weinstock, George M. Publisher: Chapman & Hall, New York, N. Y.  
CODEN: 65KVAK  
DT Conference  
LA English  
AB The authors present phys. and genetic maps of \*\*\*Borrelia\*\*\* burgdorferi isolate Sh-2-82.  
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 18 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 11  
AN 1997:344497 BIOSIS  
DN PREV199799643700  
TI Characterization of cp18, a naturally truncated member of the cp32 family of \*\*\*Borrelia\*\*\* burgdorferi plasmids.  
AU Stevenson, Brian [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ; Van Vugt, Rene; Porcella, Stephen F.; Tilly, Kit; Bono, James L.; Rosa, Patricia  
CS Lab. Microbial Structure Function, Rocky Mountain Lab., NIAID, NIH, 903 S. Fourth St., Hamilton, MT 59840, USA  
SO Journal of Bacteriology, (1997) Vol. 179, No. 13, pp. 4285-4291.  
CODEN: JOBAAY. ISSN: 0021-9193.  
DT Article  
LA English  
ED Entered STN: 11 Aug 1997  
Last Updated on STN: 11 Aug 1997  
AB We have mapped the genes encoding the antigenic lipoproteins OspE and OspF

to an approximately 18-kb circular plasmid in \*\*\*Borrelia\*\*\* burgdorferi N40. Sequencing and restriction mapping have revealed that this plasmid, cp18, is homologous to an 18-kb region of the cp32 circular plasmids found in the Lyme disease spirochetes. Our data show that cp18 may have arisen from an ancestral cp32 plasmid by deletion of a 14-kb region of DNA, indicating that a significant portion of the cp32 plasmid is not essential in cis for plasmid maintenance. These findings suggest that a relatively small recombinant plasmid capable of being stably maintained in *B. burgdorferi* could be constructed from a cp32 plasmid.

L14 ANSWER 19 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 12

AN 1998:5384 BIOSIS

DN PREV19980005384

TI Telomeres of the linear chromosomes of Lyme disease spirochaetes:  
Nucleotide sequence and possible exchange with linear plasmid telomeres.

AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]; Murphy, Maria; Delange,  
Michael; Sampson, Laura; Vugt, Rene Van; Huang, Wai Mun

CS Div. Mol. Biol. Genet., Dep. Oncol. Sci., Univ. Utah Med. Sch., Salt Lake  
City, UT 84132, USA

SO Molecular Microbiology, (Nov., 1997) Vol. 26, No. 3, pp. 581-596. print.  
CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

OS Genbank-AF08217; Genbank-AF08218; Genbank-AF08219

ED Entered STN: 23 Dec 1997

Last Updated on STN: 23 Dec 1997

AB Bacteria of the spirochaete genus \*\*\*Borrelia\*\*\* have linear  
chromosomes about 950 kbp in size. We report here that these linear  
chromosomes have covalently closed hairpin structures at their termini  
that are similar but not identical to those reported for linear plasmids  
carried by these organisms. Nucleotide sequence analysis of the  
chromosomal telomeric regions indicates that unique, apparently functional  
genes lie within a few hundred bp of each of the telomeres, and that there  
is an imperfect 26 bp inverted repeat at the two telomeres. In addition,  
we characterize a major chromosomal length polymorphism within the right  
telomeric regions of various \*\*\*Borrelia\*\*\* isolates, and show that  
sequences similar to those near the right telomere are often found on  
linear plasmids in *B. burgdorferi* (sensu stricto) isolates from nature.  
Sequences similar to a number of other regions of the chromosome,  
including those near the left telomere, were not found on *B. burgdorferi*  
plasmids. These observations suggest that there has been historical  
exchange of genetic information between the linear plasmids and the right  
end of the linear chromosome.

L14 ANSWER 20 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 13

AN 1998:46985 BIOSIS

DN PREV199800046985

TI Genomic sequence of a Lyme disease spirochaete, \*\*\*Borrelia\*\*\*  
burgdorferi.

AU Fraser, Claire M. [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ; Huang,  
Wai Mun; Sutton, Granger G.; Clayton, Rebecca; Lathigra, Raju; White,  
Owen; Ketchum, Karen A.; Dodson, Robert; Hickey, Erin K.; Gwinn, Michelle;  
Dougherty, Brian; Tomb, Jean-Francois; Fleischmann, Robert D.; Richardson,  
Delwood; Peterson, Jeremy; Kerlavage, Anthony R.; Quackenbush, John;  
Salzberg, Steven; Hanson, Mark; Van Vugt, Rene; Palmer, Nanette; Adams,  
Mark D.; Gocayne, Jeannine; Weidman, Janice; Utterback, Teresa; Watthey,  
Larry; McDonald, Lisa; Artiach, Patricia; Bowman, Cheryl; Garland, Stacey;  
Fujii, Claire; Cotton, Matthew D.; Horst, Kurt; Roberts, Kevin; Hatch,  
Bonnie; Smith, Hamilton O.; Venter, J. Craig

CS Inst. Genomic Res., 9712 Medical Center Drive, Rockville, MD 20850, USA

SO Nature (London), (Dec. 11, 1997) Vol. 390, No. 6660, pp. 580-586. print.  
CODEN: NATUAS. ISSN: 0028-0836.

DT Article

LA English

ED Entered STN: 27 Jan 1998

Last Updated on STN: 27 Jan 1998

AB The genome of the bacterium \*\*\*Borrelia\*\*\* burgdorferi B31, the aetiologic agent of Lyme disease, contains a linear chromosome of 910,725 base pairs and at least 17 linear and circular plasmids with a combined size of more than 533,000 base pairs. The chromosome contains 853 genes encoding a basic set of proteins for DNA replication, transcription, translation, solute transport and energy metabolism, but, like Mycoplasma genitalium, it contains no genes for cellular biosynthetic reactions. Because B. burgdorferi and M. genitalium are distantly related eubacteria, we suggest that their limited metabolic capacities reflect convergent evolution by gene loss from more metabolically competent progenitors. Of 430 genes on 11 plasmids, most have no known biological function; 39% of plasmid genes are paralogues that form 47 gene families. The biological significance of the multiple plasmid-encoded genes is not clear, although they may be involved in antigenic variation or immune evasion.

L14 ANSWER 21 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 14

AN 1997:438238 BIOSIS

DN PREV199799737441

TI The \*\*\*Borrelia\*\*\* burgdorferi circular plasmid cp26: Conservation of plasmid structure and targeted inactivation of the ospC gene.

AU Tilly, Kit [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ; Stevenson, Brian; Bono, James L.; Samuels, D. Scott; Hogan, Daniel; Rosa, Patricia

CS Lab. Microbial Structure Function, Natl. Inst. Allergy Infect. Dis., Rocky Mountain Lab., 903 S. 4th St., Hamilton, MT 59840, USA

SO Molecular Microbiology, (1997) Vol. 25, No. 2, pp. 361-373.

CODEN: MOMIEE. ISSN: 0950-382X.

DT Article

LA English

ED Entered STN: 8 Oct 1997

Last Updated on STN: 8 Oct 1997

AB The 26 to 28 kb circular plasmid of B. burgdorferi sensu lato (cp26) is ubiquitous among bacteria of this group and contains loci implicated in the mouse-tick transmission cycle. Restriction mapping and Southern hybridization indicated that the structure of cp26 is conserved among isolates from different origins and culture passage histories. The cp26 ospC gene encodes an outer surface protein whose synthesis within infected ticks increases when the ticks feed, and whose synthesis in culture increases after a temperature upshift. Previous studies of ospC coding sequences showed them to have stretches of sequence apparently derived from the ospC genes of distantly related isolates by homologous recombination after DNA transfer. We found conservation of the promoter regions of the ospC and guaA genes, which are divergently transcribed. We also demonstrated that the increase in OspC protein after a temperature upshift parallels increases in mRNA levels, as expected if regulatory regions adjoin the conserved sequences in the promoter regions. Finally, we used directed insertion to inactivate the ospC gene of a non-infectious isolate. This first example of directed gene inactivation in S. burgdorferi shows that the OspC protein is not required for stable maintenance of cp26 or growth in culture.

L14 ANSWER 22 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 15

AN 1997:86803 BIOSIS

DN PREV199799378516

TI Homology throughout the multiple 32-kilobase circular plasmids present in Lyme disease spirochetes.

AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]; Van Vugt, Rene; Tilly, Kit; Rosa, Patricia A.; Stevenson, Brian

CS Div. Mol. Biol. Genet., Dep. Oncol. Sci., Univ. Utah, Salt Lake City, UT 84132, USA

SO Journal of Bacteriology, (1997) Vol. 179, No. 1, pp. 217-227.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

OS Genbank-U42598; Genbank-U44912; Genbank-U44913; Genbank-U44914;



Genbank-U60639; Genbank-U60640; Genbank-U60641; Genbank-U60642;  
Genbank-U60963; Genbank-U60964; Genbank-U60965; Genbank-U72996;  
Genbank-U72997; Genbank-U72998; Genbank-U72999; Genbank-U73000;  
Genbank-U73001

ED Entered STN: 26 Feb 1997

Last Updated on STN: 2 Apr 1997

AB We have characterized seven different 32-kb circular plasmids carried by \*\*\*Borrelia\*\*\* burgdorferi isolate B31. Restriction endonuclease recognition site mapping and partial sequencing of these plasmids indicated that all seven are probably closely related to each other throughout their lengths and have substantial relationships to cp8.3, an 8.3-kb circular plasmid of B. burgdorferi sensu lato isolate Ip21. With the addition of the seven 32-kb plasmids, this bacterial strain is known to carry at least 10 linear and 9 circular plasmids. Variant cultures of B. burgdorferi B31 lacking one or more of the 32-kb circular plasmids are viable and, at least in some cases, infectious. We have examined a number of different natural isolates of Lyme disease \*\*\*borreliae\*\*\* and found that all of the B. burgdorferi sensu stricto isolates and most of the B. burgdorferi sensu lato isolates tested appear to carry multiple 32-kb circular plasmids related to those of B. burgdorferi B31. The ubiquity of these plasmids suggests that they may be important in the natural life cycle of these organisms. They may be highly conjugative plasmids or prophage genomes, which could prove to be useful in genetically manipulating B. burgdorferi.

L14 ANSWER 23 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 16

AN 1996:537157 BIOSIS

DN PREV199699259513

TI Directed insertion of a selectable marker into a circular plasmid of \*\*\*Borrelia\*\*\* burgdorferi.

AU Rosa, Patricia [Reprint author]; Samuels, D. Scott; Hogan, Daniel; Stevenson, Brian; \*\*\*Casjens, Sherwood\*\*\*; Tilly, Kit

CS Rocky Mountain Lab., 903 S. 4th St., Hamilton, MT 59840, USA

SO Journal of Bacteriology, (1996) Vol. 178, No. 20, pp. 5946-5953.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 10 Dec 1996

Last Updated on STN: 10 Dec 1996

AB Studies of the biology of \*\*\*Borrelia\*\*\* burgdorferi and the pathogenesis of Lyme disease are severely limited by the current lack of genetic tools. As an initial step toward facile genetic manipulation of this pathogenic spirochete, we have investigated gene inactivation by allelic exchange using a mutated \*\*\*borrelial\*\*\* gyrB gene that confers resistance to the antibiotic coumermycin A-1 as a selectable marker. We have transformed B. burgdorferi by electroporation with a linear fragment of DNA in which this selectable marker was flanked by sequences from a native \*\*\*borrelial\*\*\* 26-kb circular plasmid. We have identified coumermycin A-1-resistant transformants in which gyrB had interrupted the targeted site on the 26-kb plasmid via homologous recombination with the flanking sequences. Antibiotic resistance conferred by the mutated gyrB gene on the plasmid is dominant, and transformed spirochetes carrying this plasmid do not contain any unaltered copies of the plasmid. Coumermycin A-1 resistance can be transferred to naive B. burgdorferi by transformation with \*\*\*borrelial\*\*\* plasmid DNA from the initial transformants. This work represents the first example of a directed mutation in B. burgdorferi whereby a large segment of heterologous DNA (gyrB) has been inserted via homologous recombination with flanking sequences, thus demonstrating the feasibility of specific gene inactivation by allelic exchange.

L14 ANSWER 24 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
DUPLICATE 17

AN 1996:331996 BIOSIS

DN PREV199699054352

TI Analysis of linear plasmid dimers in \*\*\*Borrelia\*\*\* burgdorferi sensu

lato isolates: Implications concerning the potential mechanisms of linear plasmid replication.

AU Marconi, Richard T. [Reprint author]; \*\*\*Casjens, Sherwood\*\*\* ; Munderloh, Ulrike G.; Samuels, D. Scott

CS Dep. Microbiol. Immunol., Med. Coll. Virginia, Virginia Commonwealth Univ., Richmond, VA 23298-0678, USA

SO Journal of Bacteriology, (1996) Vol. 178, No. 11, pp. 3357-3361.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 26 Jul 1996

Last Updated on STN: 26 Jul 1996

AB The \*\*\*Borrelia\*\*\* genome is composed of a linear chromosome and a number of variable circular and linear plasmids. Atypically large linear plasmids of 92 to 105 kb have been identified in several \*\*\*Borrelia\*\*\* burgdorferi sensu lato isolates and characterized. These plasmids carry the p27 and ospAB genes, which in other isolates reside on a 50-kb plasmid. Here we demonstrate that these plasmids are dimers of the 50-kb ospAB plasmid (pAB50). The 94-kb plasmid from isolate VS116, pVS94, was an exception and did not hybridize with any plasmid gene probes. When this plasmid was used as a probe, homologous sequences in other isolates were not detected, suggesting that it is unique to isolate VS116. These analyses provide insight into the mechanism of linear plasmid replication and the mechanisms by which plasmid variability can arise.

L14 ANSWER 25 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 18

AN 1995:313474 BIOSIS

DN PREV199598327774

TI Linear Chromosomes of Lyme Disease Agent Spirochetes: Genetic Diversity and Conservation of Gene Order.

AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]; Delange, Michael; Levy, Herbert L. II; Rosa, Patricia; Huang, Wai Mun

CS Dep. Oncol. Sci., Div. Mol. Biol. Genet., Univ. Utah Med. Cent., Salt Lake City, UT 84132, USA

SO Journal of Bacteriology, (1995) Vol. 177, No. 10, pp. 2769-2780.

CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 30 Jul 1995

Last Updated on STN: 30 Jul 1995

AB We have constructed physical and genetic maps of the chromosomes of 21 Lyme disease agent spirochetes from geographically diverse locations. All have linear chromosomes whose lengths range from 935 to 955 kbp, and all contain multiple linear plasmids in the 16- to 175-kbp size range. The locations of 11 gene clusters on the chromosomes of these different isolates are indistinguishable at the resolution achieved in this study, indicating that the members of this related group of species have highly conserved chromosomal gene orders. However, chromosomal restriction endonuclease cleavage site maps are unique for nearly all isolates. The 22 chromosomal maps currently available define eight classes of Lyme disease agents. Four of these correspond to the previously proposed species \*\*\*Borrelia\*\*\* burgdorferi, \*\*\*Borrelia\*\*\* garinii, \*\*\*Borrelia\*\*\* afzelii, and \*\*\*Borrelia\*\*\* japonica. In addition, the North American isolates 21038, DN127 c19-2, 25015, and CA55 typify four additional chromosomal types that are as phylogenetically distinct as the species listed above. These findings support the idea that comparison of restriction maps is currently the most robust and definitive method for determining overall chromosomal relationships among closely related bacteria. In the course of this work, we located on the chromosome the previously unmapped outer surface protein-encoding LA7 gene and genes homologous to the Escherichia coli priA, plsC, parE, and parC genes, and we have substantially refined the locations of the recA, fla, p22A, and flgE genes.

L14 ANSWER 26 OF 26 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 19

AN 1993:409251 BIOSIS  
DN PREV199396074976  
TI Linear chromosomal physical and genetic map of \*\*\*Borrelia\*\*\*  
burgdorferi, the Lyme disease agent.  
AU \*\*\*Casjens, Sherwood\*\*\* [Reprint author]; Huang, Wai Mun  
CS Dep. Cellular, Viral Molecular Biol., Univ. Utah Med. Cent., Salt Lake  
City, UT 84132, USA  
SO Molecular Microbiology, (1993) Vol. 8, No. 5, pp. 967-980.  
CODEN: MOMIEE. ISSN: 0950-382X.  
DT Article  
LA English  
OS DDBJ-L12711; EMBL-L12711; Genbank-L12711  
ED Entered STN: 8 Sep 1993  
Last Updated on STN: 8 Sep 1993  
AB A physical map of the 952 kbp chromosome of \*\*\*Borrelia\*\*\* burgdorferi  
Sh-2-82 has been constructed. Eighty-three intervals on the chromosome,  
defined by the cleavage sites of 15 restriction enzymes, are delineated.  
The intervals vary in size from 96 kbp to a few hundred bp, with an  
average size of 11.5 kbp. A striking feature of the map is its linearity;  
no other bacterial groups are known to have linear chromosomes. The two  
ends of the chromosome do not hybridize with one another, indicating that  
there are no large common terminal regions. The chromosome of this strain  
was found to be stable in culture; passage 6, 165 and 320 cultures have  
identical chromosomal restriction maps. We have positioned all previously  
known \*\*\*Borrelia\*\*\* burgdorferi chromosomal genes and several newly  
identified ones on this map. These include the gyrA/gyrB/dnaA/dnaN gene  
cluster, the rRNA gene cluster, fla, flgE, groEL (hsp60), recA, the  
rho/hip cluster, the dnaK (hsp70)/dnaJ/grpE cluster, the pheT/pheS  
cluster, and the genes which encode the potent immunogen proteins p22A,  
p39 and p83. Our electrophoretic analysis detects five linear and at  
least two circular plasmids in B. burgdorferi Sh-2-82. We have  
constructed a physical map of the 53 kbp linear plasmid and located the  
operon that encodes the two major outer surface proteins ospA and opsB on  
this plasmid. Because of the absence of functional genetic tools for this  
organism, these maps will serve as a basis for future mapping, cloning and  
sequencing studies of B. burgdorferi.